

1600

1648

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/976,736

DATE: 01/14/2002

TIME: 18:44:34

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JAN 24 2002
TECH CENTER 1600/2900

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1 <110> APPLICANT: Bass, Michael B
2 Sullivan, John K
3 Theill, Lars E
4 Wang, Daguang
5 <120> TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
6 <130> FILE REFERENCE: A-548
7 <140> CURRENT APPLICATION NUMBER: US/09/976,736
8 <141> CURRENT FILING DATE: 2001-10-09
10 <150> PRIOR APPLICATION NUMBER: US/09/161,241
11 <151> PRIOR FILING DATE: 1998-09-25
14 <160> NUMBER OF SEQ ID NOS: 78
15 <170> SOFTWARE: PatentIn Ver. 2.0
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18 <211> LENGTH: 1050
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20 <213> ORGANISM: Mouse
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24 cctcaggagg aagctacgct caatgagatg tttcgagagg tggaggagct gatggaagac 180
25 actcagcaca aactgcgcag tgccgtggag gagatggagg cggaagaagc agctgctaaa 240
26 acgtcctctg aggtgaacct ggcaagctta cctcccaact atcacaatga gaccagcacg 300
27 gagaccaggg tgggaaataa cacagtccat gtgcaccagg aagttcacia gataaccaac 360
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34 tgccatgacc ccaccagcca gctgtctggat ctcatacctt gggaactgga gcctgaagga 780
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48 ccgcaggagg aggccacct caatgagatg ttccgcgagg ttgaggaact gatggaggac 180
49 acgcagcaca aattgcgcag cgcggtggaa gagatggagg cagaagaagc tgctgctaaa 240
50 gcatcatcag aagtgaacct ggcaaacctta cctccagct atcacaatga gaccaacaca 300
51 gacacgaagg ttggaataa taccatccat gtgcaccgag aaattcacia gataaccaac 360
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54      tttgccagct tccagtacac ctgccagcca tgccggggcc agaggatgct ctgcaccccg 540
55      gacagtgagt gctgtggaga ccagctgtgt gtctggggtc actgcaccaa aatggccacc 600
56      aggggcagca atgggacat ctgtgacaac cagagggact gccagccggg gctgtgctgt 660
57      gccttcaga gaggcctgct gttccctgtg tgacacccc tgcccggtga gggcgagctt 720
58      tgccatgacc ccgccagccg gcttctggac ctcatcacct gggagctaga gcctgatgga 780
59      gccttgacc gatgcccttg tgccagtggc ctctctgccc agccccacag ccacagcctg 840
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61      cccagagagg tccccgatga gtatgaagtt ggcagcttca tggaggagggt gcgccaggag 960
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72      gctatcaaga acctgcccc accgctgggc ggcgctgcgg ggcacccagg ctctgcagtc 180
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74      cagccgtacc cgtgcgcaga ggacgaggag tgcggcactg atgagtactg cgtagtccc 300
75      acccgcgag gggacgcggc cgtgcaaata tgtctgcct gcaggaagcg ccgaaaacgc 360
76      tgcatgcgtc acgctatgtg ctgccccggg aattactgca aaaatggaat atgtgtgtct 420
77      tctgatcaaa atcatttccg aggagaaatt gaggaacca tcaactgaaag ctttggtaat 480
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79      accaaaggac aagaaggttc tgtttgtctc cggatcatcag actgtgcctc aggattgtgt 600
80      tgtgctagac acttctggtc caagatctgt aaacctgtcc tgaaagaagg tcaagtgtgt 660
81      accaagcata ggagaaaagg ctctcatgga ctagaaatat tccagcgttg ttactgtgga 720
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91      ctgatggtgg agagctcaca gctaggcagc tcgcgggcca aactcaactc catcaagtcc 120
92      tctctaggag gggagactcc tgctcagtca gccaacgat ctgcaggcat gaaccaagga 180
93      ctggctttcg gcggcagtaa gaaggcaaaa agcctggggc aggcctacct ttgcagcagt 240
94      gataaggaat gtgaagttgg aagatactgc cacagtcccc accaaggatc atcagcctgc 300
95      atgctctgta ggaggaaaaa gaaacgatgc cacagagatg ggatgtgttg ccctgggtacc 360
96      cgctgcaata atggaatctg catcccagtc actgagagca tcctcacccc acatatccca 420
97      gctctggatg gcacccggca tagagatcgc aaccatggtc actattccaa ccatgacctg 480
98      ggatggcaga atctaggaag gccacactcc aagatgcctc atataaaagg acatgaagga 540
99      gacccatgcc tacggtcatc agactgcatt gatgggtttt gttgtgctcg ccacttctgg 600
100     accaaaatct gcaaaccagt gctccatcag ggggaagtct gtaccaaaca acgcaagaag 660
101     ggttcgcacg ggctggagat tttccagagg tgtgactgtg caaaggcctc gtcctgcaaa 720
102     gtgtggaaag atgccaccta ctcttccaaa gccagactcc atgtatgcca gaagatctga 780
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111      tctctgggcg gggagacgcc tggtcaggcc gccaatcgat ctgcggggcat gtaccaagga 180
112      ctggcattcg gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 240
113      gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc atcggcctgc 300
114      atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg gcatgtgctg cccagttacc 360
115      cgctgcaata atggcatctg tatcccagtt actgaaagca tottaacccc tcacatcccc 420
116      gctctggatg gtactcggca cagagatcga aaccacggtc attactcaaa ccatgacttg 480
117      ggatggcaga atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 540
118      gacccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg tcatttctgg 600
119      accaaaatct gcaaacacgt gctccatcag ggggaagtct gtaccaaaca acgcaagaa 660
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130      tctctgggcg gggagacgcc tggtcaggcc gccaatcgat ctgcggggcat gtaccaagga 180
131      ctggcattcg gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 240
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135      ttttgcgtgt ctcgtcattt ctggaccaa atctgcaaac cagtgtctca tcagggggaa 480
136      gtctgtacca aacaacgcaa gaagggttct catgggctgg aaattttcca gcgttgcgac 540
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147      tgcctgtctg acacggactg caataccaga aagttctgcc tccagccccg cgatgagaag 180
148      ccgttctgtg ctacatgtcg tgggttgagg aggaggtgcc agcgagatgc catgtgctgc 240
149      cctgggacac tctgtgtgaa cgatgtttgt actacgatgg aagatgcaac cccaatatta 300
150      gaaaggcagc ttgatgagca agatggcaca catgcagaag gaacaactgg gcacccagtc 360
151      caggaaaacc aacccaaaag gaagccaagt attaagaaat cacaaggcag gaagggacaa 420
152      gagggagaaa gttgtctgag aacttttgac tgtggccctg gactttgctg tgctcgtcat 480
153      ttttgacga aaatttgtaa gccagtcctt ttggagggac aggtctgctc cagaagaggg 540
154      cataaagaca ctgctcaagc tccagaaatc ttccagcgtt gcgactgtgg ccctggacta 600
155      ctgtgtcgaa gccaatgac cagcaatcgg cagcatgctc gattaagagt atgccccaaa 660

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166      20          25          30
167      Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
168      35          40          45
169      Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
170      50          55          60
171      Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
172      65          70          75          80
173      Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
174      85          90          95
175      Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His
176      100         105         110
177      Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe
178      115         120         125
179      Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser
180      130         135         140
181      His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln
182      145         150         155         160
183      Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met
184      165         170         175
185      Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp
186      180         185         190
187      Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys
188      195         200         205
189      Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
190      210         215         220
191      Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
192      225         230         235         240
193      Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu
194      245         250         255
195      Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
196      260         265         270
197      Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe
198      275         280         285
199      Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala
200      290         295         300
201      Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu
202      305         310         315         320
203      Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly
204      325         330         335
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216 20 25 30
217 Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
218 35 40 45
219 Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
220 50 55 60
221 Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
222 65 70 75 80
223 Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
224 85 90 95
225 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
226 100 105 110
227 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
228 115 120 125
229 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
230 130 135 140
231 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
232 145 150 155 160
233 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
234 165 170 175
235 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
236 180 185 190
237 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
238 195 200 205
239 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
240 210 215 220
241 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
242 225 230 235 240
243 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
244 245 250 255
245 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
246 260 265 270
247 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
248 275 280 285
249 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
250 290 295 300
251 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
252 305 310 315 320
253 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
254 325 330 335
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VERIFICATION SUMMARY

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